

Index

A

- AAA domain-containing protein 3 (ATAD3),
 - functional overview, 87
- N*-Acetylcysteine (NAC), ethylmalonic encephalopathy management, 218
- Aft1, 202–203
- Aft2, 202–203
- AHS. *See* Alpers-Huttenlocher syndrome
- Aldehyde dehydrogenase 2 (ALDH2),
 - SIRT3 regulation, 257
- ALDH2. *See* Aldehyde dehydrogenase 2
- Alex3, neuron mitochondria trafficking regulation, 173
- Alpers-Huttenlocher syndrome (AHS)
 - clinical features, 95–96
 - POLG defect characterization, 96–101
- AMP-activated protein kinase (AMPK)
 - mitochondrial biogenesis signaling, 115
 - therapeutic targeting, 121
- AMPK. *See* AMP-activated protein kinase
- ANS. *See* Ataxia neuropathy spectrum
- Apoptosis. *See also* Mitochondrial outer membrane permeabilization
 - Bak activation, 185–186
 - Bax activation and oligomerization, 183–185
 - Bcl-2 protein interactions, 180–182
- ATAD3. *See* AAA domain-containing protein 3
- Ataxia neuropathy spectrum (ANS)
 - clinical features, 96
 - POLG defect characterization, 96–101
- Atm1, 202
- Autophagy
 - collagen VI muscle disease defects, 228–229
 - SIRT1 regulation, 255

B

- Bacterial dynamin-like protein (BDLP),
 - evolution, 137–138
- Bak
 - Bcl-2 protein interactions in mitochondria, 180–182
 - mitochondrial outer membrane permeabilization role, 181, 185–187
 - pore formation by oligomers, 186–188
- BamA, SAM complex, 69–70
- Bax
 - Bcl-2 protein interactions in mitochondria, 180–182
 - mitochondrial outer membrane permeabilization role, 181, 183–185

- pore formation by oligomers, 186–188
- Bcl-2 proteins, interactions in mitochondria, 180–182
- BDLP. *See* Bacterial dynamin-like protein
- Beclin 1, levels in collagen VI muscle diseases, 228
- Bethlem myopathy. *See* Collagen VI
- Biogenesis, mitochondria
 - fusion and fission machinery interactions, 118
 - microtubule dynamics, 119
 - mitophagy triggering, 118–119
 - nuclear transcriptional complexes regulating mitochondrial gene expression
 - CREB, 114
 - estrogen-related receptors, 113–114
 - nuclear respiratory factor 1, 112
 - nuclear respiratory factor 2, 112
 - peroxisome proliferator-activated receptor- γ , 112–113
 - peroxisome proliferator-activated receptor- γ coactivator-1, 114
 - sirtuins, 114–115
 - thyroid hormone receptor, 113
 - YY1, 114
- peripheral mitochondria maintenance
 - in neurons, 165
- protein import to mitochondria, 119–120
- signaling
 - AMP-activated protein kinase, 115
 - calcium flux, 115–117
 - mechanistic target of rapamycin, 116–117
 - protein kinase A, 116
 - reactive oxygen species, 117
 - retrograde signaling, 117
 - therapeutic targeting, 120–122
 - transcription machinery, 120
 - unfolded protein response and quality control, 117–118
- Bnip3, levels in collagen VI muscle diseases, 228
- BOLA
 - BOLA3 mutation and disease, 205
 - iron–sulfur protein synthesis, 199
- Bone marrow transplantation, ethylmalonic encephalopathy management, 218

C

- Calcium flux
 - mitochondrial biogenesis signaling, 115–117
 - neuron mitochondria trafficking regulation, 170–171

Index

- Cancer
- metabolic properties of tumor cells, 236
 - mitochondrial respiration decrease, 236–238
 - oncocytic tumor
 - mitochondrial DNA mutations
 - overview, 219–220
 - structural and functional consequences, 244–245
 - mitochondrial hyperplasia and compensatory effect hypothesis, 243
 - origin and fate, 246
 - overview of features, 241–242
 - prospects for study, 245, 247
 - reactive oxygen species
 - enhanced production, 238
 - mitochondrial dysfunction induction, 238
 - supercomplex organization loss and effects
 - cancer cell studies, 241
 - coenzyme Q channeling loss, 240
 - individual complex stability and assembly loss, 240
 - overview, 238–239
 - phospholipid peroxidation and supercomplex formation prevention, 239–240
 - reactive oxygen species increase, 240–241
- Carbamoyl phosphate synthetase 1 (CPS-1), SIRT5 regulation, 258
- Carbonic anhydrase, mitochondrial proteome evolution, 11, 12
- Cardiolipin, mitochondrial outer membrane permeabilization role, 188
- CBS. *See* Cystathione β -synthase
- Cfd1, iron–sulfur protein synthesis, 199–200
- Charcot-Marie-Tooth disease (CMT), mitofusin mutations, 137
- Cia1, iron–sulfur protein synthesis, 201
- Cia2, iron–sulfur protein synthesis, 201
- CMT. *See* Charcot-Marie-Tooth disease
- Collagen VI
- assembly, 224
 - functions, 223–224
 - muscle diseases
 - autophagy defects, 228–229
 - Bethlem myopathy, 224–225
 - congenital myosclerosis, 225
 - cyclosporin A therapy and mitochondrial effects, 226–227, 230
 - knockout mouse studies, 225–226, 228
 - Ulrich congenital muscular dystrophy, 225
 - zebrafish studies, 229–230
 - structure, 223–224
- Complex I
- evolution, 10–11
 - gene mutations, 24–25
 - Parkin mutations, 144–145
 - Parkinson disease dysfunction, 143
 - PINK1 mutations, 144–145
 - reactive oxygen species, cancer, supercomplex organization loss, and effects
 - cancer cell studies, 241
 - coenzyme Q channeling loss, 240
 - individual complex stability and assembly loss, 240
 - overview, 238–239
 - phospholipid peroxidation and supercomplex formation prevention, 239–240
 - reactive oxygen species increase, 240–241
- Congenital myosclerosis. *See* Collagen VI
- COX. *See* Cytochrome *c* oxidase
- CPS-1. *See* Carbamoyl phosphate synthetase 1
- CREB
- mitochondrial gene expression regulation, 114
- CsA. *See* Cyclosporin A
- CSE. *See* Cystathione γ -lyase
- Cyclophilin D, SIRT3 deactivation, 257
- Cyclosporin A (CsA), collagen VI muscle disease management and mitochondrial effects, 226–227, 230
- Cystathione β -synthase (CBS), hydrogen sulfide synthesis, 211–212
- Cystathione γ -lyase (CSE), hydrogen sulfide synthesis, 211–212
- Cytochrome *c* oxidase (COX), inhibition by hydrogen sulfide, 217–218
- ## D
- Dehydroascorbic acid (DHA), ethylmalonic encephalopathy management, 218
- DHA. *See* Dehydroascorbic acid
- DNA polymerase- γ (POLG)
- linker region in accessory subunit binding, 101–102
 - mutation and disease
 - Alpers-Huttenlocher syndrome, 95–96
 - ataxia neuropathy spectrum, 96
 - diagnostic clinical features, 94–95
 - exonuclease activity, disease and mitochondrial DNA mutagenesis, 102–104
 - management
 - exercise attenuation of premature aging, 105–106
 - nucleotide availability targeting, 105
 - oxidative stress reduction, 104–105
 - molecular characterization of defects, 96–101
 - myocerebrohepatopathy spectrum, 95
 - myoclonic epilepsy myopathy sensory ataxia, 96
 - overview, 93–94
 - progressive external ophthalmoplegia, 96–97, 101
 - prospects for study

- nucleoid, 85–86
- structure, 93
- Drp-1
 - Bax pore formation by oligomers, 187
 - mitochondrial fission/fusion role, 129–130
 - phosphorylation, 131–132
 - receptors, 131
 - recruitment, 133
- Dynein, motor/adaptor complex for mitochondrial motility, 165–167

- E**
- EE. *See* Ethylmalonic encephalopathy
- Endoplasmic reticulum (ER), mitochondrial fusion coordination, 132–133
- Endosymbiosis. *See* Evolution, mitochondria
- ER. *See* Endoplasmic reticulum
- ERMES, mitochondrial outer membrane trafficking, 70
- ERRs. *See* Estrogen-related receptors
- Erv1, 71
- Estrogen-related receptors (ERRs), mitochondrial gene expression regulation, 113–114
- ETHE1*, ethylmalonic encephalopathy mutations, 216–217
- Ethylmalonic encephalopathy (EE)
 - pathophysiology, 215–217
 - therapeutic approaches, 217–218
- Evolution, mitochondria
 - endosymbiotic models
 - archezoa hypothesis, 5–6
 - hydrogen hypothesis, 6–7
 - overview, 5
 - fission/fusion machinery, 137–138
 - genetic and genomic analysis, 2–4
 - history of study, 1–2
 - mitochondrion-related organelles, 7–8
 - phylogenetic and phylogenomic reconstruction, 4–5
 - prospects for study, 11–12
 - proteome evolution, 8–11

- F**
- FH. *See* Fumarate hydratase
- Fis1, mitochondrial fission role, 130–131, 133
- Fission, mitochondria
 - adaptor proteins, 130–131
 - biogenesis interactions, 118
 - coordination with cytoskeleton and endoplasmic reticulum, 132–133
 - Dynamamin family member roles, 128–130
 - evolution, 137–138
 - machinery mutations and disease, 136–137
 - mtDNA heteroplasmy regulation, 48–49
 - peripheral mitochondria maintenance in neurons, 165
 - posttranslational modification of mediators, 131–132
- FtsZ, homologs, 138
- Fumarate hydratase (FH), mutation in cancer, 244–245
- Fusion, mitochondria
 - adaptor proteins, 130–131
 - biogenesis interactions, 118
 - Dynamamin family member roles, 128–130
 - evolution, 137–138
 - fusion protein functions outside fusion, 134–136
 - machinery mutations and disease, 136–137
 - mtDNA heteroplasmy regulation, 48–49
 - peripheral mitochondria maintenance in neurons, 165
 - proteolysis and ubiquitination in regulation, 133–134
- Fzo1, mitochondrial fusion role, 128–129

- G**
- GDAP1, Parkin degradation, 150, 153
- Gene therapy
 - ethics, 57–58
 - mitochondrial diseases, 54–57
- Genetic counseling, mitochondrial diseases, 50–54
- GLRX5, iron–sulfur protein synthesis, 198
- Glutaredoxin
 - iron–sulfur protein synthesis, 201, 203
 - mutation and disease, 204
- GRIM-19*, oncocytic tumor mutations, 219–220
- Grx5, iron–sulfur protein synthesis, 197–198

- H**
- Heteroplasmy, mtDNA
 - germline segregation
 - animal studies of human mutations
 - bovine, 30
 - mouse, 30–34
 - primate, 34–35
 - familial transmission of mutations, 27–28
 - low-level germline heteroplasmy, 29–30
 - mathematical description, 40–43
 - selection studies in mouse
 - deletion mutation segregation, 36
 - frameshift mutation segregation, 36–37
 - overview, 35–36
 - selection detection with mathematical models, 39
 - single-base tRNA deletion mutation segregation, 37–39
 - statistical analysis of variance, 39–40
 - variability in oocytes, 27
 - replicative segregation, 17, 19
 - segregation control by mitochondria physiological processes

Index

- Heteroplasmy, mtDNA (*Continued*)
 fission of mitochondria, 48–49
 fusion of mitochondria, 48–49
 inter-mtDNA complementation, 49
 mitophagy, 49–50
 reactive oxygen species, 46–48
 somatic segregation
 human mutations, 44–45
 mouse mutations, 45–46
 overview, 43–44
- HIF-1 α . *See* Hypoxia-inducible factor-1 α
- HUMMR, neuron mitochondria trafficking regulation, 172–173
- Hydrogen hypothesis, mitochondria symbiogenesis, 6–7
- Hydrogen sulfide
 catabolism, 212–213
 ethylmalonic encephalopathy
 pathophysiology, 215–217
 therapeutic approaches, 217–218
 physical properties, 213
 physiological functions, 214–215
 synthesis, 211–212
 toxicity, 215
- Hydrogenosome, evolution, 7–8
- Hypoxia-inducible factor-1 α (HIF-1 α), activity in cancer, 241, 246–247
- I**
- IDH2. *See* Isocitrate dehydrogenase 2
- Ind1
 iron–sulfur protein synthesis, 198–199
 mutation and disease, 204–205
- Iron–sulfur proteins
 deficiency and disease, 195, 203–205
 functional overview, 194–195
 iron homeostasis regulation by mitochondria, 202–203
 iron–sulfur cluster assembly machinery
 components, 194, 196
 export machinery, 199
 mitochondria machinery role in cytosolic and nuclear protein assembly, 199–202
 mitochondrial versus cytosolic, 194
 prospects for study, 205–206
 steps in protein assembly, 196–199
 overview, 193–194
- IRP proteins, intracellular iron regulation, 203–204
- Isa1, iron–sulfur protein synthesis, 198
- Isa2, iron–sulfur protein synthesis, 198
- Isd11, iron–sulfur protein synthesis, 197
- Isocitrate dehydrogenase 2 (IDH2), SIRT3 regulation, 256–257
- Isu1, iron–sulfur protein synthesis, 197
- J**
- Jacl, iron–sulfur protein synthesis, 197
- K**
- KBP. *See* Kinesin-binding protein
- Kinesin
 calcium regulation, 170–171
 motor/adaptor complex for mitochondrial motility, 165–168
- Kinesin-binding protein (KBP), mitochondrial motility role, 167
- Kinesin-like protein 6 (KLP6), mitochondrial motility role, 167
- KLP6. *See* Kinesin-like protein 6
- L**
- Leber hereditary optic neuropathy (LHON)
 familial transmission of mutations, 27
 gene mutations, 18
- Leigh syndrome, familial transmission of mutations, 27
- LPA. *See* Lysophosphatidic acid
- Lysophosphatidic acid (LPA), neuron mitochondria trafficking regulation, 172
- M**
- MCHS. *See* Myocerebrohepatopathy spectrum
- Mdm10, mitochondrial outer membrane trafficking, 70
- Mdv1, mitochondrial fission role, 130
- Mechanistic target of rapamycin (mTOR), mitochondrial biogenesis signaling, 116–117
- MELAS. *See* Mitochondrial encephalomyopathy, lactic acidosis, and stroke-like episodes
- MEMSA. *See* Myoclonic epilepsy myopathy sensory ataxia
- MERRE. *see* Myoclonic epilepsy and ragged red fiber disease
- Metronidazole, ethylmalonic encephalopathy management, 217–218
- Mff, mitochondrial fusion role, 131
- Mfn. *See* Mitofusin
- Mge1, iron–sulfur protein synthesis, 197
- Mgm1
 mitochondrial fusion role, 128
 proteolysis, 134
- Mia40, 71
- Milton, motor/adaptor complex for mitochondrial motility, 165–167
- Mim1, mitochondrial outer membrane trafficking, 70
- MINOS. *See* Mitochondrial inner membrane organizing system

- Miro
Miro1
mitochondria immobilization, 154–155
Parkin degradation, 154
Miro2 in mitochondria immobilization, 154–155
motor/adaptor complex for mitochondrial motility,
165–167, 171–173
- MISS. *See* Mitochondrial IMS sorting signal
- Mitochondrial DNA (mtDNA). *See also* Nucleoid
ancient adaptive polymorphisms, 20–24
control region, 19–20
haplogroup migration, 21–23
heteroplasmic alleles. *See* Heteroplasmy, mtDNA
mutation and disease. *See also specific diseases*
classes, 19
complexity, 17–18
gene therapy, 54–57
genetic counseling, 50–54
incidence, 18
maternally inherited diseases, 19–20
overview, 84
pathophysiology of complex diseases, 25–27
preimplantation genetic diagnosis, 51–54
rate of mutation, 19
somatic mutations, 24
nuclear DNA interactions, 24–25
oncogenic tumor mutations
overview, 219–220
structural and functional consequences,
244–245
overview of genes, 17, 19, 83–84
- Mitochondrial encephalomyopathy, lactic acidosis, and
stroke-like episodes (MELAS)
familial transmission of mutations, 27
preimplantation genetic diagnosis, 52–54
somatic segregation, 45
- Mitochondrial IMS sorting signal (MISS), 67
- Mitochondrial inner membrane organizing system
(MINOS), 72
- Mitochondrial neurogastrointestinal encephalopathy
(MNGIE), clinical features, 95
- Mitochondrial outer membrane permeabilization
(MOMP)
Bak role, 181, 185–187
Bax role, 181, 183–185
initiation events, 184
lipid requirements, 187–188
overview, 179–180
prospects for study, 188–189
- Mitochondrial processing peptidase (MPP), 67
- Mitochondrial RNA polymerase (POLRMT)
mitochondrial biogenesis role, 120
nucleoid, 85
- Mitochondrial targeting signal (MTS), evolution, 9
- Mitochondrion-related organelles (MROs),
evolution, 7–8
- Mitofusin (Mfn)
degradation, 133
impaired mitochondria isolation
via PINK1/Parkin, 154
Mfn1, Parkin degradation, 150, 153–154
Mfn2
mutation effects, 135
Parkin degradation, 154
mitochondrial fusion role, 128–129
mutation effects, 134, 137
- MitoNEET, Parkin degradation, 150, 153
- Mitophagy
biogenesis triggering, 118–119
mtDNA heteroplasmy regulation, 49–50
Parkin induction, 155–156
- Mitosome, evolution, 7–8
- Mms19, iron–sulfur protein synthesis, 201
- MNGIE. *See* Mitochondrial neurogastrointestinal
encephalopathy
- Mohr-Tranebjaerg syndrome (MTS), gene mutations, 76
- MOMP. *See* Mitochondrial outer membrane
permeabilization
- MOSC1, Parkin degradation, 150, 153
- Motility. *See* Neuron mitochondria trafficking
- MPP. *See* Mitochondrial processing peptidase
- MROs. *See* Mitochondrion-related organelles
- mtDNA. *See* Mitochondrial DNA
- MTERF, mitochondrial biogenesis role, 120
- mTOR. *See* Mechanistic target of rapamycin
- MTS. *See* Mitochondrial targeting signal;
Mohr-Tranebjaerg syndrome
- Myocerebrohepatopathy spectrum (MCHS)
clinical features, 95
POLG defect characterization, 96–101
- Myoclonic epilepsy and ragged red fiber disease
(MERRF), gene mutations, 18
familial transmission of mutations, 27–28
preimplantation genetic diagnosis, 52
somatic segregation, 46
- Myoclonic epilepsy myopathy sensory ataxia (MEMSA)
clinical features, 96
POLG defect characterization, 96–101

N

- NAC. *See* N-Acetylcysteine
- Nbp35, iron–sulfur protein synthesis, 199–200
- NBRI, Parkin-mediated mitophagy role, 156–157
- Nerve growth factor (NGF), neuron mitochondria
trafficking regulation, 172
- Neuron mitochondria trafficking
Alex3 regulation, 173
biological importance, 163–165
calcium regulation, 170–171
HUMMR regulation, 172–173
motor/adaptor complex, 165–167

- Neuron mitochondria trafficking (*Continued*)
 nerve growth factor regulation, 172
 OGT regulation, 172–173
 Parkin regulation, 171–172
 PINK1 regulation, 171–172
 prospects for study, 173–174
 RhoA regulation, 172
 stationary pool, 168–170
- Nfs1, iron–sulfur protein synthesis, 197
- Nfu1
 iron–sulfur protein synthesis, 198–199
 mutation and disease, 205
- NGF. *See* Nerve growth factor
- NRF-1. *See* Nuclear respiratory factor 1
- NRF-2. *See* Nuclear respiratory factor 2
- Nuclear respiratory factor 1 (NRF-1), mitochondrial
 gene expression regulation, 112
- Nuclear respiratory factor 2 (NRF-2), mitochondrial
 gene expression regulation, 112
- Nucleoid
 cellular signaling role, 89
 organellar network integration
 and dynamics, 86–88
 packaging, 85–86
 structure, 84–85
- O**
- OGT, neuron mitochondria trafficking regulation,
 172–173
- Opa-1
 mitochondrial fusion role, 128
 mutation effects, 134–136
 proteolysis, 134–135
- Ornithine transcarbamoylase, SIRT3 substrate, 256
- Outer mitochondrial membrane. *See* Mitochondrial
 outer membrane permeabilization
- OXA. *See* Oxidase assembly complex
- Oxidase assembly complex (OXA), 75
- Oxidative phosphorylation
 cancer and decrease, 236–238
 overview, 18–19
- P**
- p62/SQSTM1
 Parkin-mediated mitophagy role, 156–157
 PINK1/Parkin pathway, 150, 153
- PAM. *See* Presequence translocase-associated
 import motor
- Parkin
 impaired mitochondria isolation via mitofusins, 154
 mitochondria immobilization through
 Miro level regulation, 154–155
 mitochondrial outer membrane protein
 ubiquitination, 148
 mitophagy mechanism, 155–156
 mitophagy role, 118–119
 neuron mitochondria trafficking regulation,
 171–172
 recruitment and activation by PINK1, 145,
 147–148
 substrate identification, 148–154
 Parkinson disease (PD). *See also* Parkin; PINK1
 Complex I dysfunction, 143
 gene mutations, 143–144
 PARP. *See* Poly(ADP-ribose) polymerase
 PD. *See* Parkinson disease
 PEO. *See* Progressive external ophthalmoplegia
 Permeability transition pore (PTP)
 activation, 19
 collagen VI muscle disease studies, 227–229
 mitophagy role, 119
 Peroxisome proliferator-activated receptor- γ (PPAR- γ),
 mitochondrial gene expression
 regulation, 112–113
 Peroxisome proliferator-activated receptor- γ
 coactivator-1 (PGC-1)
 mitochondrial gene expression regulation, 114
 SIRT1 regulation, 254–255
 therapeutic targeting, 121
 PGC-1. *See* Peroxisome proliferator-activated
 receptor- γ coactivator-1
 PGD. *See* Preimplantation genetic diagnosis
 PHB1. *See* Prohibitin 1
 PHB2. *See* Prohibitin 2
 PINK1
 impaired mitochondria isolation
 via mitofusins, 154
 mitochondria immobilization through
 Miro level regulation, 154–155
 mitochondrial import, 145
 mitochondrial stress sensing, 145–146
 mitofusin degradation role, 133
 mitophagy role, 118
 neuron mitochondria trafficking regulation,
 171–172
 Parkin recruitment and activation, 145, 147–148
 PKA. *See* Protein kinase A
 POLG. *See* DNA polymerase- γ
 POLRMT. *See* Mitochondrial RNA polymerase
 Poly(ADP-ribose) polymerase (PARP), SIRT1
 regulation, 254–255
 PPAR- γ . *See* Peroxisome proliferator-activated
 receptor- γ
 Ppif, SIRT3 substrate, 257
 Preimplantation genetic diagnosis (PGD),
 mitochondrial diseases, 51–54
 Presequence translocase-associated import motor
 (PAM), 74–76
 Progressive external ophthalmoplegia (PEO)
 clinical features, 96

POLG defect characterization, 96–101
Prohibitin 1 (PHB1), functional overview, 87
Prohibitin 2 (PHB2), functional overview, 87
Protein kinase A (PKA)
 Drp1 phosphorylation, 131–132
 mitochondrial biogenesis signaling, 116
Protein trafficking, mitochondria
 intermembrane space protein import, 71–73
 mitochondrial outer membrane trafficking
 pathways, 69–71
 overview, 65–66
 precursor protein synthesis and targeting, 66–67
 prospects for study, 74–75
 TIM23 and inner membrane insertion/matrix
 translocation, 73–75
 TOM complex, 67–69
Proteomics, mitochondria proteome evolution, 8–11
PTP. *See* Permeability transition pore
Puf3, mRNA targeting to mitochondria, 67

Q

Qcr6, trafficking, 74

R

Reactive oxygen species (ROS)
 cancer
 enhanced production, 238
 mitochondrial dysfunction induction, 238
 supercomplex organization loss and effects
 cancer cell studies, 241
 coenzyme Q channeling loss, 240
 individual complex stability and assembly
 loss, 240
 overview, 238–239
 phospholipid peroxidation and
 supercomplex formation prevention,
 239–240
 reactive oxygen species increase, 240–241
 mitochondrial biogenesis signaling, 117
 mtDNA heteroplasmy regulation, 46–48
RhoA, neuron mitochondria trafficking
 regulation, 172
ROS. *See* Reactive oxygen species

S

SAM complex, mitochondrial outer membrane
 trafficking, 70–71
SAR11 clade, 4
SCAD. *See* Short-chain acylCoA dehydrogenase
SDH. *See* Succinate dehydrogenase
Short-chain acylCoA dehydrogenase (SCAD),
 deficiency in ethylmalonic
 encephalopathy, 215, 217

SIMH. *See* Stress-induced mitochondrial
 hyperperfusion
Sirtuins
 mitochondrial gene expression regulation,
 114–115
 prospects for mitochondrial function studies,
 258–259
 SIRT1 mitochondrial function, 254–256
 SIRT3 mitochondrial function, 256–258
 SIRT5 mitochondrial function, 258
 therapeutic targeting, 121
 types and functional overview, 253–254
Ssq1, iron–sulfur protein synthesis, 197
Stress-induced mitochondrial hyperperfusion
 (SIMH), 137
Succinate dehydrogenase (SDH), mutation in cancer,
 244–245
Sulfide. *See* Hydrogen sulfide
Symbiosis. *See* Evolution, mitochondria
Syntaphilin, mitochondria anchoring, 169

T

TFAM. *See* Transcription factor A mitochondrial
TFB2M, mitochondrial biogenesis role, 120
Thyroid hormone receptor, mitochondrial gene
 expression regulation, 113
TIM chaperones. *See also* TOM complex
 mitochondrial biogenesis role, 119
 mitochondrial outer membrane trafficking, 70
 TIM22 complex and intermembrane space protein
 import, 72–73
 TIM23 and inner membrane insertion/matrix
 translocation, 73–75
TOM complex
 outer membrane protein biogenesis, 68
 prospects for study, 74–75
 regulation, 69
 structure, 68
 TIM22 complex and intermembrane space protein
 import, 72–73
 TIM23 and inner membrane insertion/matrix
 translocation, 73–75
 Tom70, Parkin degradation, 150, 153
Trafficking. *See* Neuron mitochondria trafficking;
 Protein trafficking, mitochondria
TRAK1, motor/adaptor complex for mitochondrial
 motility, 166, 173
TRAK2, motor/adaptor complex for mitochondrial
 motility, 166, 173
Transcription factor A mitochondrial (TFAM)
 mitochondrial biogenesis role, 120
 nuclear respiratory factor 1 regulation of
 expression, 112
 nucleoid function, 85–88

Index

Translocase of outer membrane complex.

See TOM complex

Twinkle, nucleoid, 86

U

UCP2. *See* Uncoupling protein-2

Ugo1, mitochondrial fusion role, 131

Ulrich congenital muscular dystrophy. *See* Collagen VI

Uncoupling protein-2 (UCP2), SIRT1 regulation,
255–256

V

VDAC. *See* Voltage-dependent anion channel

Voltage-dependent anion channel (VDAC)

Bak interactions, 187

Parkin-mediated mitophagy role, 156

Y

Yah1, iron–sulfur protein synthesis, 197

YY1, mitochondrial gene expression regulation, 114